

Asn Thr Pro Cys Ser Glu Asn Lys Leu Asp Ile Gln Glu Lys Lys Leu
 130 135 140

Ile Asn Gln Glu Lys Lys Met Phe Arg Ile Arg Asn Arg Ser Tyr Ile
 145 150 155 160

Asp Arg Asp Ser Glu Tyr Leu Leu Gln Glu Asn Glu Pro Asp Gly Thr
 165 170 175

Leu Asp Gln Lys Leu Leu Glu Asp Leu Gln Lys Lys Lys Asn Asp Leu
 180 185 190

Arg Tyr Ile Glu Met Gln His Phe Arg Glu Lys Leu Pro Ser Tyr Gly
 195 200 205

Met Gln Lys Glu Leu Val Asn Leu Ile Asp Asn His Gln Val Thr Val
 210 215 220

Ile Ser Gly Glu Thr Gly Cys Gly Lys Thr Thr Gln Val Thr Gln Phe
 225 230 235 240

Ile Leu Asp Asn Tyr Ile Glu Arg Gly Lys Gly Ser Ala Cys Arg Ile
 245 250 255

Val Cys Thr Gln Pro Arg Arg Ile Ser Ala Ile Ser Val Ala Glu Arg
 260 265 270

Val Ala Ala Glu Arg Ala Glu Ser Cys Gly Ser Gly Asn Ser Thr Gly
 275 280 285

Tyr Gln Ile Arg Leu Gln Ser Arg Leu Pro Arg Lys Gln Gly Ser Ile
 290 295 300

Leu Tyr Cys Thr Thr Gly Ile Ile Leu Gln Trp Leu Gln Ser Asp Pro
 305 310 315 320

Tyr Leu Ser Ser Val Ser His Ile Val Leu Asp Glu Ile His Glu Arg
 325 330 335

Asn Leu Gln Ser Asp Val Leu Met Thr Val Val Lys Asp Leu Leu Asn
 340 345 350

Phe Arg Ser Asp Leu Lys Val Ile Leu Met Ser Ala Thr Leu Asn Ala
 355 360 365

Glu Lys Phe Ser Glu Tyr Phe Gly Asn Cys Pro Met Ile His Ile Pro
 370 375 380

Gly Phe Thr Phe Pro Val Val Glu Tyr Leu Leu Glu Asp Val Ile Glu
 385 390 395 400

Lys Ile Arg Tyr Val Pro Glu Gln Lys Glu His Arg Ser Gln Phe Lys
 405 410 415

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Asn Ile Ser Trp Lys Lys Thr Ile Val Thr Arg Phe Leu Lys Leu Val
1 5 10 15

Pro Asp Leu Leu Ala Ile Val Gln Arg Lys Lys Glu Gly Glu Glu
20 25 30

Glu Gln Ala Ile Asn Arg Gln Thr Ala Leu Tyr Thr Leu Lys Leu Leu
35 40 45

Cys Lys Asn Phe Gly Ala Glu Asn Pro Asp Pro Phe Val Pro Val Leu
50 55 60

Ser Thr Ala Val Lys Leu Ile Ala Pro Glu Arg Lys Glu Glu Lys Asn
65 70 75 80

Val Leu Gly Ser Ala Leu Leu Cys Met Ala Glu Val Thr Ser Thr Leu
85 90 95

Glu Ala Leu Ala Ile Pro Gln Leu Pro Ser Leu Met Pro Ser Leu Leu
100 105 110

Thr Thr Met Lys Asn Thr Ser Glu Leu Val Ser Ser Glu Val Tyr Leu
115 120 125

Leu Ser Ala Leu Ala Ala Leu Gln Lys Val Val Glu Thr Leu Pro His
130 135 140

Phe Ile Ser Pro Tyr Leu Glu Gly Ile Leu Ser Gln Val Ile His Leu
145 150 155 160

Glu Lys Ile Thr Ser Glu Met Gly Ser Ala Ser Gln Ala Asn Ile Arg
165 170 175

Leu Thr Ser Leu Lys Thr Leu Ala Thr Thr Leu Ala Pro Arg Val
180 185 190

Leu Leu Pro Ala Ile Lys Lys Thr Tyr Lys Gln Ile Glu Lys Asn Trp
195 200 205

Lys Asn His Met Gly Pro Phe Met Ser Ile Leu Gln Glu His Ile Gly
210 215 220

Ala Met Lys Lys Glu Glu Leu Thr Ser His Gln Ser Gln Leu Thr Ala
225 230 235 240

Phe Phe Leu Glu Ala Leu Asp Phe Arg Ala Gln His Ser Glu Asn Asp
245 250 255

Leu Glu Glu Val Gly Lys Thr Glu Asn Cys Ile Ile Asp Cys Leu Val
260 265 270

Ala Met Val Val Lys Leu Ser Glu Val Thr Phe Arg Pro Leu Phe Phe
275 280 285

Lys Leu Phe Asp Trp Ala Lys Thr Glu Asp Ala Pro Lys Asp Arg Leu
290 295 300

Leu Thr Phe Tyr Asn Leu Ala Asp Cys Ile Ala Glu Lys Leu Lys Gly
305 310 315 320

Leu Phe Thr Leu Phe Ala Gly His Leu Val Lys Pro Phe Ala Asp Thr
325 330 335

Leu Asp Gln Val Asn Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser
 340 345 350
 Glu Asn Asp Pro Glu Lys Cys Cys Leu Leu Leu Gln Phe Ile Leu Asn
 355 360 365
 Cys Leu Tyr Lys Ile Phe Leu Phe Asp Thr Gln His Phe Ile Ser Lys
 370 375 380
 Glu Arg Ala Gly Ala Leu Met Met Pro Leu Val Asp Gln Leu Glu Asn
 385 390 395 400
 Arg Leu Gly Gly Glu Lys Phe Gln Glu Arg Val Thr Lys His Leu
 405 410 415
 Ile Pro Cys Ile Ala Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu
 420 425 430
 Trp Lys Pro Leu Asn Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser
 435 440 445
 Pro Lys Val Arg Phe Ala Ala Leu Ile Thr Val Leu Ala Leu Ala Glu
 450 455 460
 Lys Leu Lys Glu Asn Tyr Ile Val Leu Leu Pro Glu Ser Ile Pro Phe
 465 470 475 480
 Leu Ala Glu Leu Met Glu Asp Glu Cys Glu Glu Val Glu His Gln Cys
 485 490 495
 Gln Lys Thr Ile Gln Gln Leu Glu Thr Val Leu Gly Glu Pro Leu Gln
 500 505 510
 Ser Tyr Phe
 515

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Gly Val Val Pro Asn Gly Arg Asp Ala Glu Ser Gly His Ser Leu Ala
 1 5 10 15
 Glu Gly Gln Ala Pro His Gly Leu Pro Gly Thr Pro Gly Ala Ser Gly
 20 25 30
 Gly Val Val Leu Gln Pro Arg Gly Arg Arg Arg Ala Asp Pro Pro His
 35 40 45
 Arg Gln Leu Arg Pro Glu Ala Phe Gly Asn His Arg Arg Ser Glu Phe
 50 55 60
 Leu Arg Leu Gln Val Glu Gly Gly Cys Ser Gly Phe Gln Tyr Lys
 65 70 75 80
 Phe Ser Leu Asp Thr Val Ile Asn Pro Asp Asp Arg Val Phe Glu Gln
 85 90 95